



SEQUENCE LISTING

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Torensma, Ruurd

<120> COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL
INTERACTION

<130> 89 DIV

<140> US 10/625,202

<141> 2003-07-23

<150> 09/719,961

<151> 2001-09-24

<150> PCT/NL00/00253

<151> 2000-04-19

<150> US 60/176,924

<151> 2000-01-20

<150> EP 99201204.7

<151> 1999-04-19

<160> 2

<170> PatentIn version 3.2

<210> 1

<211> 1215

<212> DNA

<213> Homo sapiens

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48

gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag
Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys
20 25 30

96

agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc
Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
35 40 45

144

tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc
Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
50 55 60

192

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ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa tcc aag Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys 85 90 95	288
ctg cag gag atc tac cag gag ctg acc cag ctg aag gct gca gtg ggt Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly 100 105 110	336
gag ctt cca gag aaa tct aag ctg cag gag atc tac cag gag ctg acc Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr 115 120 125	384
cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag ctg cag Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln 130 135 140	432
gag atc tac cag gag ctg acc tgg ctg aag gct gca gtg ggt gag ctt Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu 145 150 155 160	480
cca gag aaa tct aag atg cag gag atc tac cag gag ctg act cgg ctg Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu 165 170 175	528
aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile 180 185 190	576
tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu 195 200 205	624
aaa tct aag cag cag gag atc tac cag gag ctg acc cgg ctg aag gct Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala 210 215 220	672
gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc tac cag Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln 225 230 235 240	720
gag ctg acc cag ctg aag gct gca gtg gaa cgc ctg tgc cac ccc tgt Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys 245 250 255	768
ccc tgg gaa tgg aca ttc ttc caa gga aac tgt tac ttc atg tct aac Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn 260 265 270	816
tcc cag cgg aac tgg cac gac tcc atc acc gcc tgc aaa gaa gtg ggg Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly 275 280 285	864

gcc cag ctc gtc gta atc aaa agt gct gag gag cag aac ttc cta cag Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln 290 295 300	912
ctg cag tct tcc aga agt aac cgc ttc acc tgg atg gga ctt tca gat Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp 305 310 315 320	960
cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc tca cct ctg ttg Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu 325 330 335	1008
ccc agc ttc aag cag tat tgg aac aga gga gag ccc aac aac gtt ggg Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly 340 345 350	1056
gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg aac gac gac aaa Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys 355 360 365	1104
tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Ser Ala Ala Ser Cys 370 375 380	1152
tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct gcc acc cca aac Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn 385 390 395 400	1200
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Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro 50 55 60

Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
65 70 75 80

Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
85 90 95

Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
100 105 110

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
115 120 125

Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
130 135 140

Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu
145 150 155 160

Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
165 170 175

Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile
180 185 190

Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
195 200 205

Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala
210 215 220

Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
225 230 235 240

Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys
245 250 255

Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
260 265 270

Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly
275 280 285

Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
290 295 300

Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
305 310 315 320

Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
325 330 335

Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
340 345 350

Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
355 360 365

Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
370 375 380

Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
385 390 395 400

Pro Pro Pro Ala